L Number	Hits	Search Text	DB	Time stamp
1	0	"200123604"	USPAT;	2003/10/22
2	2	"200123604"	US-PGPUB USPAT;	16:34 2003/10/22
			US-PGPUB; EPO;	16:39
3	175	coli same (verotoxin or vtl or "vt 1")	DERWENT USPAT;	2003/10/22
			US-PGPUB; EPO;	16:42
	82	(asli sama (sanatasin an setl an Uset 18))	DERWENT	2003/10/22
4	82	<pre>(coli same (verotoxin or vtl or "vt 1")) same (pcr detect\$ oligonucleotide align\$</pre>	USPAT; US-PGPUB;	16:43
		amplif\$)	EPO; DERWENT	

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OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 16:27:49; Search time 377.273 Seconds

(without alignments)

2168.703 Million cell updates/sec

Title: US-10-085-056-24

Perfect score: 20

Sequence: 1 tgtaacgtggtatagctact 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

identical search repeated in GENSEQ, USPATS, USPGPUBS, and EST databases

SID2

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OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 16:27:49; Search time 377.273 Seconds

(without alignments)

2168.703 Million cell updates/sec

Title: US-10-085-056-2

Perfect score: 20

Sequence: 1 tggcgatttatctgcatccc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

SVD 15

OM nucleic - nucleic search, using sw model

Run on: September 10, 2003, 16:27:49; Search time 471.591 Seconds

(without alignments)

2168.703 Million cell updates/sec

Title: US-10-085-056-15

Perfect score: 25

Sequence: 1 tttttatcgctttgctgatttttca 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

KI